

FIG. 15 CONTINUED

ClaI
 |
 AAGT G G A A

361 TGGGGGATGTGAAGGAAATCAGAAATCGATTGAGTCCCTCGAAGAATGCAAGAAGATGTG 420
 -----+-----+-----+-----+-----+-----+-----+
 ACCCCCTACACTTCCTTTAGTCTTAGCTAAACTCAGGGAGCTTCTTACGTTCTTCTACAC
 GlyGlyCysGluGlyAsnGlnAsnArgPheGluSerLeuGluGluCysLysLysMetCys -
 75

421 T AA A T T
 CACCCGCGACAACGCAAACAGGATTATAAAGACAACATTGCAACAAGAAAAGCCAGATTT 480
 -----+-----+-----+-----+-----+-----+-----+
 GTGGGCGCTGTTGCGTTTGTCTAATATTTCTGTTGTAACGTTGTTCTTTTCGGTCTAAA
 ThrArgAspAsnAlaAsnArgIleIleLysThrThrLeuGlnGlnGluLysProAspPhe -

481 CTGCTTTTTTGAAGAAGATCCTGGAATATGTCGAGGTTATATTACCAGGTATTTTTTATAA 540
 -----+-----+-----+-----+-----+-----+-----+
 GACGAAAAACCTTCTTCTAGGACCTTATACAGCTCCAATATAATGGTCCATAAAAAATATT
 CysPheLeuGluGluAspProGlyIleCysArgGlyTyrIleThrArgTyrPheTyrAsn -

541 CAATCAGACAAAACAGTGTGAACGTTTCAAGTATGGTGGATGCCTGGGCAATATGAACAA 600
 -----+-----+-----+-----+-----+-----+-----+
 GTTAGTCTGTTTGTGCACACTTGCAAAGTTCATACCACCTACGGACCCGTTATACTTGTT
 AsnGlnThrLysGlnCysGluArgPheLysTyrGlyGlyCysLeuGlyAsnMetAsnAsn -

601 TTTTGAGACACTGGAAGAATGCAAGAACATTTGTGAAGATGGTCCGAATGGTTTCCAGGT 660
 -----+-----+-----+-----+-----+-----+-----+
 AAAACTCTGTGACCTTCTTACGTTCTTGTAAACACTTCTACCAGGCTTACCAAAGGTCCA
 PheGluThrLeuGluGluCysLysAsnIleCysGluAspGlyProAsnGlyPheGlnVal -

661 GGATAATTATGGAACCCAGCTCAATGCTGTGAATAACTCCCTGACTCCGCAATCAACCAA 720
 -----+-----+-----+-----+-----+-----+-----+
 CCTATTAAATACCTTGGGTCGAGTTACGACACTTATTGAGGGACTGAGGCGTTAGTTGGTT
 AspAsnTyrGlyThrGlnLeuAsnAlaValAsnAsnSerLeuThrProGlnSerThrLys -

721 GGTTCCCGAGCCTTTTTGAATTTACGGTCCCTCATGGTGTCTCACTCCAGCAGACAGAGG 780
 -----+-----+-----+-----+-----+-----+-----+
 CCAAGGGTCGAAAAACTTAAAGTGCCAGGGAGTACCACAGAGTGAGGTCGTCTGTCTCC
 ValProSerLeuPheGluPheHisGlyProSerTrpCysLeuThrProAlaAspArgGly -

781 ATTGTGTCGTGCCAATGAGAACAGATTCTACTACAATTCAGTCATTGGGAAATGCCGCC 840
 -----+-----+-----+-----+-----+-----+-----+
 TAACACAGCACGGTTACTCTTGTCTAAGATGATGTTAAGTCAGTAACCCTTTACGGCGGG
 LeuCysArgAlaAsnGluAsnArgPheTyrTyrAsnSerValIleGlyLysCysArgPro -

FIG. 15 CONTINUED

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ATTTAAAGTACAGTAGGATGTGGGGGAAATGAAAACAATTTTACTTCCAAACAAGAATGTCT
841 -----+-----+-----+-----+-----+-----+-----+ 900
TAAATTTCATGTCACCTACACCCCTTTACTTTTGTTAAATGAAGGTTTGTTCTTACAGA

PheLysTyrSerGlyCysGlyGlyAsnGluAsnAsnPheThrSerLysGlnGluCysLeu -

GAGGGCATGTAAAAAAGGTTTTCATCCAAAGAATATCAAAAGGAGGCCTAATTAAACCAA
901 -----+-----+-----+-----+-----+-----+-----+ 960
CTCCCGTACATTTTTTCCAAGTAGGTTTCTTATAGTTTCTCCGGATTAATTTTGTT

ArgAlaCysLysLysGlyPheIleGlnArgIleSerLysGlyGlyLeuIleLysThrLys -

                                C terminus of Ala-TFPI coding sequence
AAGAAAAAGAAAGAAGCAGAGAGTGAAAATAGCATATGAAGAAATTTTTGTAAAAATAT
961 -----+-----+-----+-----+-----+-----+-----+ 1020
TTCITTTTTCTTCTTCGTCTCTCACTTTTATCGTATACTTCTTTAAAAACAATTTTATA

ArgLysArgLysLysGlnArgValLysIleAlaTyrGluGluIlePheValLysAsnMet -

      Stop   HindIII
      TGA^^^AAGCTT (in pMON6655)
          |
          | Translation Termination
          | HindIII ClaI
                                     EcoRI   EcoRV   P22 term delta
      GTAATAAAAAGCTTATCGATGATAAGCTGTCAAACATGAGAATTCGATATCAACGCAACGA
1021 -----+-----+-----+-----+-----+-----+-----+ 1080
      CATTATTTTTCGAATAGCTACTATTTCGACAGTTTGTACTCTTAAGCTATAGTTGCCGTTGCT

      EndEnd

                                   EcoRV   EcoRI
                                   |       |
      GCCAGCCGAAGCTGGGTCGTTGCGTTGATATCGAATTC
1081 -----+-----+-----+-----+-----+-----+-----+ 1118
      GGGTCGGCTTCGACCCAGCAACGCAACTATAGCTTAAG

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